



What's New at NCBI?

Recent updates for NCBI resources

<https://www.ncbi.nlm.nih.gov/> <https://ncbiinsights.ncbi.nlm.nih.gov/>

National Center for Biotechnology Information • National Library of Medicine • National Institutes of Health • Department of Health and Human Services

The National Center for Biotechnology Information (NCBI) provides databases and analysis tools for the research community from the NCBI homepage at www.ncbi.nlm.nih.gov. To help you keep up with changes at NCBI, we publish an annual update in the special database issue of *Nucleic Acids Research* that provides an updated description of databases, services, and tools available from NCBI. You can find all published updates by searching PubMed (go.usa.gov/xpb9t). The current document highlights some of the most recent developments.

Literature Resources

We have released some new features for PubMed (pubmed.ncbi.nlm.nih.gov/):

- A new user guide (pubmed.ncbi.nlm.nih.gov/help/) answers many common questions about how best to use the new site.
- Additional links on the new PubMed homepage helps your navigation by connecting to other popular sites at NCBI, such as [E-utilities](#), [Advanced Search](#), and the [MeSH database](#).
- The action menu now contains *Collections* and *My Bibliography*, allowing you to manage and share groups of citations. After running a search, you will also find a “Create alert” link under the search box that lets you set up automatic My NCBI email updates for your search.

See this blogpost for more details: go.usa.gov/xpWQC

MyNCBI

We released a new interface for My Bibliography, the bibliographical management tool in MyNCBI. This update streamlines creating and updating your own bibliography collection for grant reporting. See the YouTube tutorial here for more details: youtu.be/DDHkAVQ5dDQ. Next January, National Science Foundation will join existing funding agencies, National Institutes of Health and Health Research Alliance, in using My Bibliography for reporting by grantees.

Human Genetics Resource

ClinVar

We have updated the ClinVar display to the Varinat-centric view. This display aggregates the clinical assertions for different conditions and displays them under the “Conditions” tab. The new display helps make it clear same variant impacts different conditions in different ways. See this blogpost for details and specific examples: go.usa.gov/xpDBm

dbSNP

Later this year we plan to release aggregated population-based allele frequency data from dbGaP studies. The initial release, dubbed ALFA, will add the dbGaP-derived population allele frequency to the top of the existing “Frequency” section of a SNP record. A brief description of this is at: go.usa.gov/xpWCP

Sequence Analysis Tools & Sequence Data in the Cloud

- Our BLAST group has released Docker images for its sequence analysis package BLAST, that can be readily installed for use in a cloud environment: github.com/ncbi/docker/tree/master/blast
- The Prokaryotic Genome Annotation Pipeline (PGAP) software package is also available to the public as a Docker package: github.com/ncbi/pgap
- The Genome Data Viewer, NCBI’s genome browser, now offers in-browser sequence downloads and adding remote track hubs from registered third party providers. See: www.ncbi.nlm.nih.gov/genome/gdv/browser/release-notes/
- As a participant of the NIH STRIDES Initiative (datascience.nih.gov/strides), NCBI has made the key BLAST databases and all of its next-gen sequence data in its Sequence Read Archive available from participating cloud providers (Google and Amazon).

Other Updates

For more news and updates, check out our blogposts: ncbiinsights.ncbi.nlm.nih.gov/